

PRIMARY HIV-1 ISOLATE

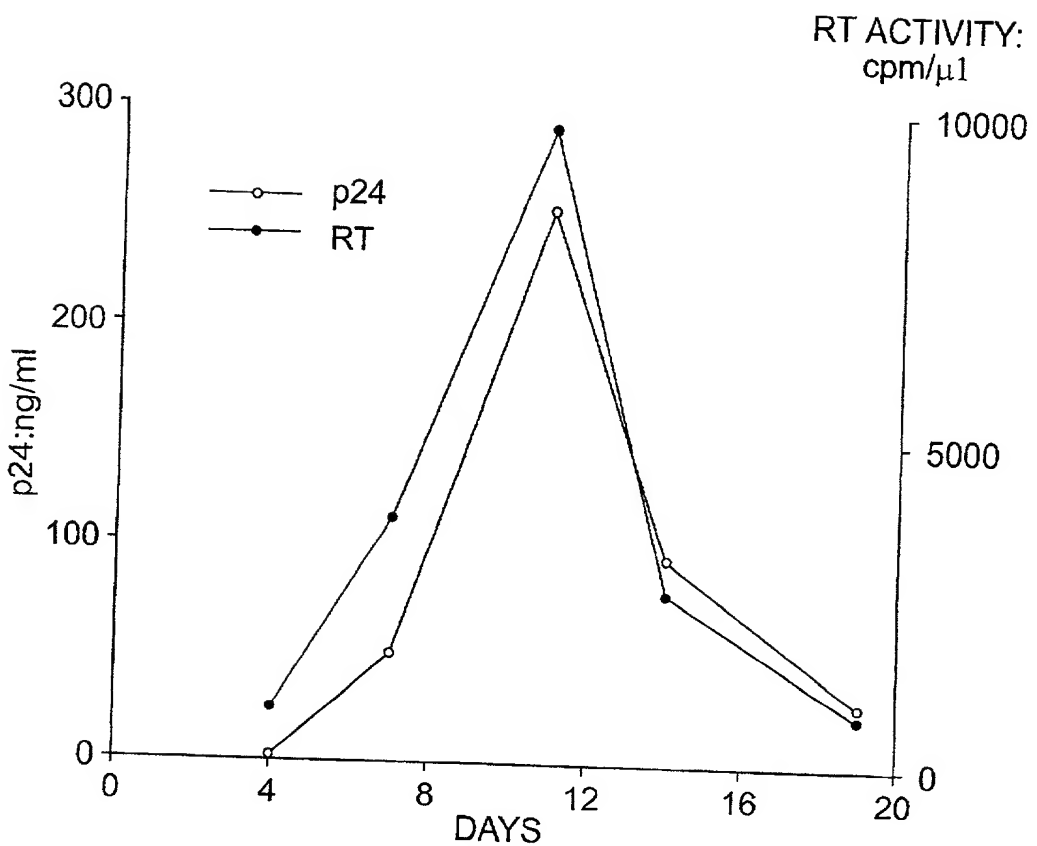


FIG. 1A

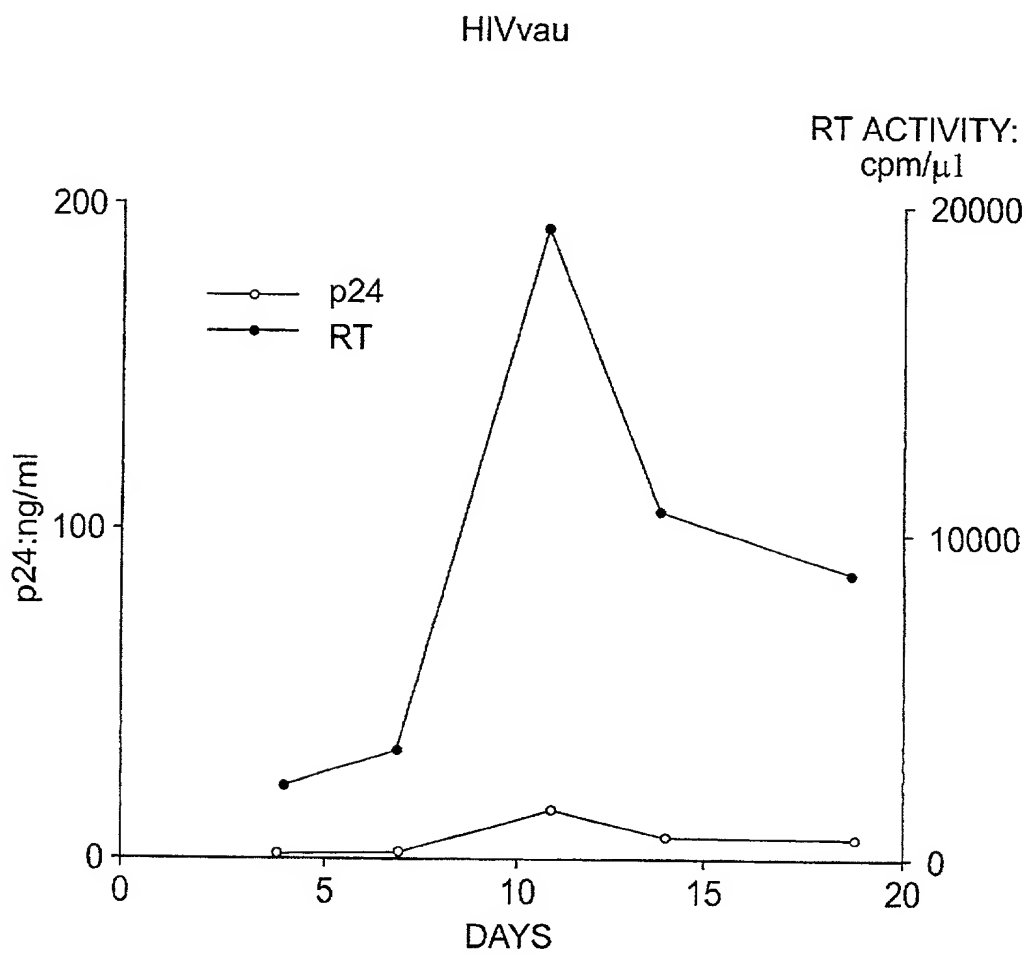


FIG. 1B

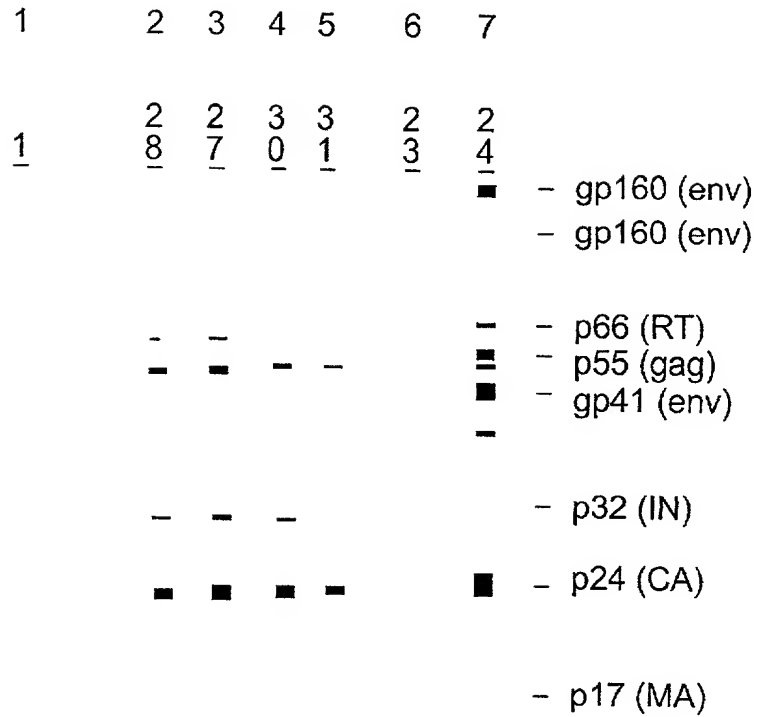


FIG. 2

SIGNAL PEPTIDE

VAU	1	..MTAIMKAMGKRNRKLGIWCLILALIIPCLSCNQLYATVYSGVPVWEDA	48
		... : : : : : : : : : : ... : : : :	
LAI	1	MRVKEKYQHLWRWGKKG..TMLLGILMICSATEKLWVTVYYGVPVWKEA	48
VAU	49	KPTLFCASDANLTSTEQHNIWATQACVPTDPSNEYELKNVTGKFNIWKN	98
		.. . : : . . : . :	
LAI	49	TTTLFCASDAKAYDTEVHNWVATHACVPTDPNPQEVVLNVNVTENFNMWKN	98
VAU	99	YIVDQMHEDIIDLWDQSLKPCVQMTFLCVQMCTDIKNSINTNSPLNSN	148
		: : . : : . : . .	
LAI	99	DMVEQMHEDIISLWDQSLKPCVKLTPLCVSLKCTDLGNATNTNSSNTNSS	148
VAU	149	NTK.....EVKQCDFNVTTVLKDKQEKQALFYVTDLVKINATSNETMY	192
		... : . . : . : : : : . : : : .	
LAI	149	SGEMTMEKGEIKNCSFNISTSRGKVQKEYAFFYKLDIIPID..NDTTSY	196

FIG. 3A

FIG. 3B

VAU 441 SGLYAPPPIPGNLVCRSNITGMILQLDTPWNKTHPNSTLPPGGGDMKDIW 490
 LAI 437 KAMYAPPISGQIRCSSNITGLLLTRDGGNNNN..GSEIFRPGGGDMRDNW 484
 GP120 ← GP41

VAU 491 RTQLFKYKVVVRVKPFSVAPTkiARPTIGTRSHREKRAAGLAMLFLGILSA 540
 LAI 485 RSELYKYKVKIEPLGVAPTkaRRV....QREKRAVGIGALFLGFLGA

VAU 541 AGSTMGAAATALTVRTOHLIKGIVQQQDNLLRAIQQQHLLRPSVWGIRQ 590
 LAI 531 AGSTMGARSMTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQ 580

IMMUNODOMINANT EPITOPE

VAU 591 LRARLLALETFIQNQQLLNWGCCKNRLICYTSVKWNKTWGGDN.ESIWDE 639
 LAI 581 LQARILAVEERYLKDQQLGIWGC SGKLICTTAVPWNASWSNKSLEQIWNN 630

FIG. 3C

FIG. 3D

HIV-1lai	RILAVERYLKDQQLGIWGCSGKLIC
HIV-1Z321	-----I--
HIV-1eli	-----H--
HIV-1JRCSF	-V-----M-----
HIV-1WMJ	-V-----R-----
HIV-1NDK	-V-----R-----RH--
HIV-1mal	-V-----Q--R--M-----H--
SIVCPZGAB	-L-----Q---I--L-----AV-
vau	-L--L-TFIQN---NL---KNR---
mvp5180	-LQ-L-TLIQN--R-NL---K-----
ant70	-L--L-TL-QN---SL---K---V-
HIV-2rod	-VT-I-K--Q--AR-NS---AFRQV-
HIV-2D194	-VT-I-K-----AQ-NS---AFRQV-

FIG. 4

FIG. 5A

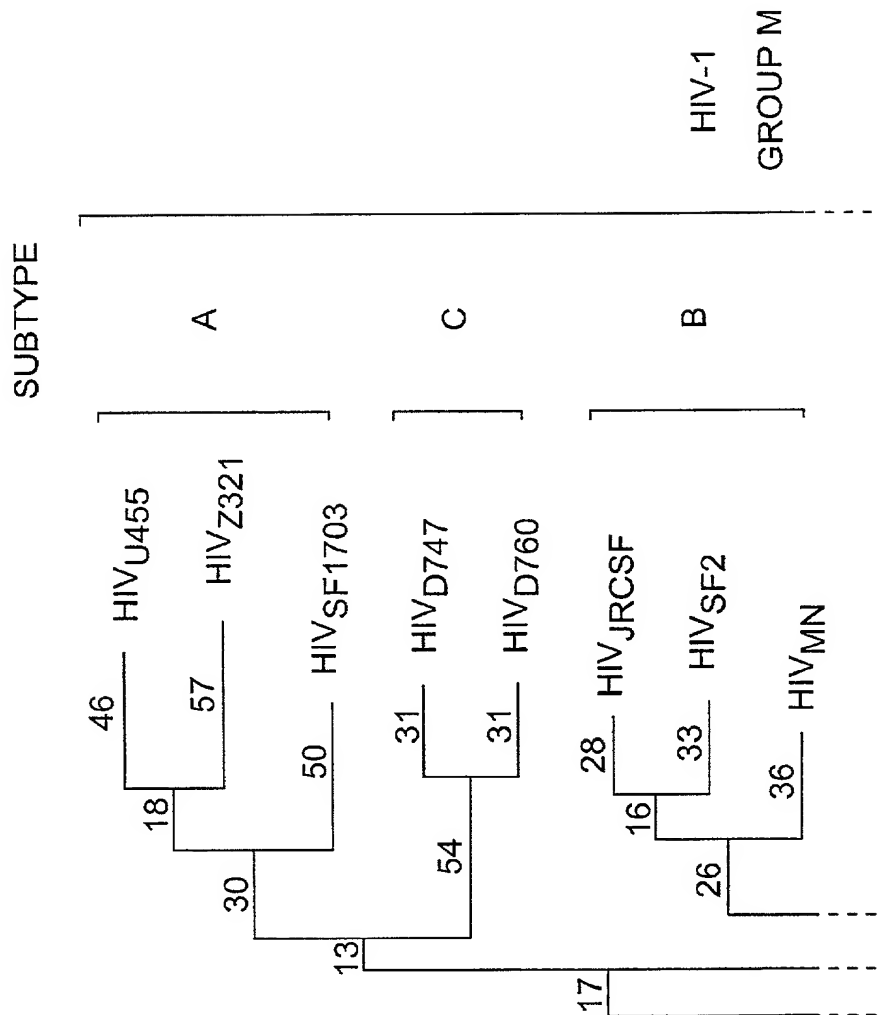
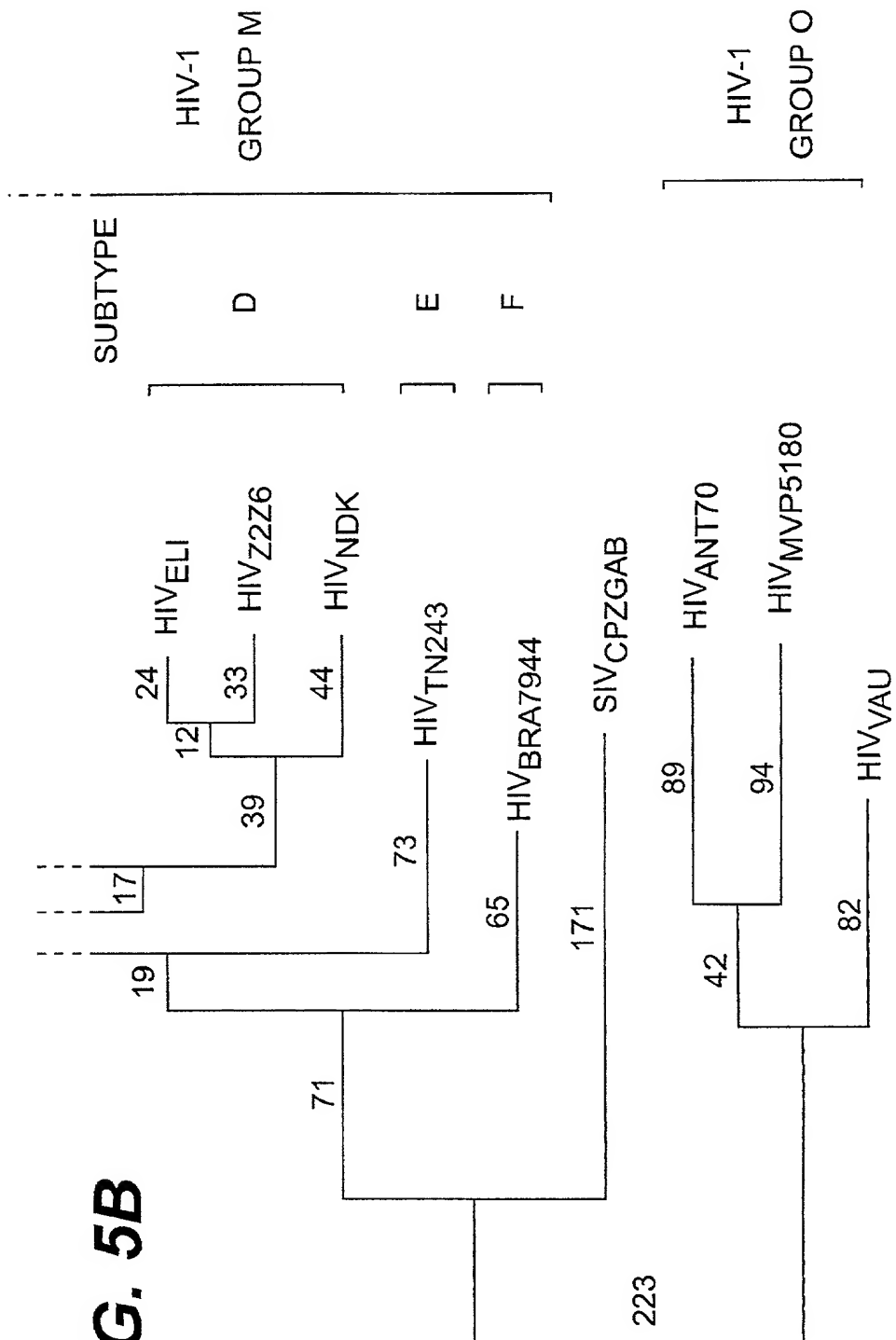


FIG. 5B



DNA SEQUENCE 2631 B.P. ATGACAGGATT ... CGACTCCTGTGTTA LINEAR									
10	20	30	40	50	60	70	80	90	100
1 ATGACAGCGA TTATGAAGC AATGGGGAAG AGGAACAGGA AGTTAGGGAT	CTGGTGCTTG ATTTTGGCTT TGATAATCCC ATGTTTGAGC TGTAACCAAC								
101 TATATGCCAC AGTCTATTCT GGGGTACCTG TATGGGAAGA TGCAAAACCA	ACATTGTTCT GTGCTTCAGA TGCTAACTTG ACAAGCACTG AACAGCATAA								
201 TATTTGGGCA ACACAAGCCT GTGTCTCCAC AGACCCCACT CCAATGAAT	ATGAGCTAAA AAATGTGACA GGTAAATTC AATATATGAA AAATATATA								
301 GTAGACCAAA TGCACGAAGA CATTATAGAT TTGTGGGACC AGAGTTAAA	ACCTTGTTGT CAAATGACIT TCTTGTGTGT ACAAATGAAT TGTACAGATA								
401 TCAAAAATAG TATTAAATACC ACAAACAGTC CCTTAAACTC AAACAATACA	AAAGAGGTGA AACAGTGTGA CTTTAAATGA ACTACAGTGC TCAAAGACAA								
501 ACAGGAGAAA AAACAGGCTC TATTCTATGT GACAGATTG GTTAAGATTA	ACGCCACATC AAATGAAACA ATGTATAGAT TAATTAATG TAACCTCACA								
601 ACCATCAGC AGGCTCTCTC AAAGCTATCT TTTGAGCCCA TTCCCATACA	CTATTGTGCT CCAGCGGGAT GTGCCATCTT TAAGTGTAA GAAACAGGAT								
701 TTAATGGAAC AGGTCTCTGT AAAACAGTTA CAGTAGTTAC TTGTACACAT	GGCATCAAA CAACAGTAAG TACCCAACTA ATACTAAATG GGACACTCTC								
801 TAAAGGAAT ATAACATCA TGGGAAGAA TATTTAGCA AGTGGGAGA	ACATCTTAAT AACCTTAAAT ACTAATATA CAATAGCATG TGAGAGACCA								
901 GGAATCAGA CAATACAAA GATATGGCA GGTCCAATGG CTTGTGTACAG	CATGGCCCTT AGTAATACAA AGGGGGATAC AAGGGCAGCT TATTGTAAAT								
1001 ATAGTGGT TGAATGCAAG AAGCTTAA AAAACATAA TGAAGATAT	TTAGAAGCTT TAGAATATAA TCAAACTGAT GTTTTAATCA TACCTTTTCC								
1101 TCACAGTGGT GAAGATGCAG AAGTAACAAA TTTCTTTTCT AACTGTCTAG	GAGAAATCTT TTATTGTAAC ACAAACTGGC TGTTTAATCA TACCTTTTCC								
1201 TCGAAGAAGA ATATGACCA TAACAGATC AATTGTACTA ATATTGCAA	TAATAGCAAT GGCACCTCAG CAATACCTTG CAGGTTGAGA CAAGTAGTAA								
1301 GGGACTCGAT GAGGGGAGGA TCGGGACTTT ATGCACCTCC CATCCAGGA	AACCTAGTAT GCAGGTCAA CATAACTGGA ATGATTTCTAC AATTGGACAC								
1401 GCCATGGAAT AAAACATC CTAACAGCAC CACCCTTAGA CCAGGAGGG	GAGATATGAA AGATATATGG AGAACTCAAT TGTTCAAAATA TAAAGTAGTA								
1501 AGAGTAAAC CTTTATAGT AGCAACAACA AAAATTGCAA GGCCAACTAT	AGGAACTAGA TCTCATAGAG AGAAAAGAGC ACCAGGTTG GCAATGCTAT								
1601 TCTTGGGGAT TCTAAGTGCA GCAGGAAGCA CTATGGGCGC AGCGGCAACA	GGCTGACGG TACGGACCCA GCATCTGATA AAGGTATAG TGAACACAGA								
1701 GGATAACCTG CTAAGAGCAA TACAGGCCCA GCAACACTTG CTGAGGCCAT	CTGTATGGGG TATTAGACAA CTCCGAGCTC GCCTGCTAGC CTTAGAAACC								
1801 TTTATACAGA ATCAGCAACT CCTTAACCTG TGGGGCTGCA AGAATAGACT	AATCTGCTAC ACATCAGTAA AGTGGAAATA AACATGGGGA GGAGATAATG								
1901 AATCAATTG GGATGAGTTA ACATGCGAGC AGTGGGATCA ACAGATAAAC	AACGTAAGCT CCTTCATATA TGAAAAATA CAAGAGGCAC AAGAACAACA								
2001 GGAGAAAAT GAGAAAGAT TGCTGGAGTT AGATGAATGG GCCTCTATT	GGAAATGGCT TGACATAACT AACATTAGGC AGGGATATCA ACCCTCTCTG TTACAGATCC								
2101 ATCATAGTAG GAGCACTAAT AGGTCTAAGA GTAGTTATGA TAGTACTTAA	TCTACTAAAG AACATTAGGC AGGATATCA ACCCTCTCTG TTACAGATCC								
2201 CCATCCAACA ACAAGCGGA GTAGGAACGC CAGGAGGAAC AGGAGAAGGA	GGTGGAGACG AAGACAGGCG CAGGTGGACT CAGATCCAGA ACACCTGGGA								
2301 GCATCTGTTG TACACGGACC TCAGGACAAT AATCTTGTGG ATTTACCACC	TCTTGAGCAA CTTAGCCTCA GAGATCCAGA AGTTGATCAG ACACCTGGGA								
2401 CTTGGACTAT GGATCATAGG GCAGAGGACA AATTGAAGCTT GCAGACTCTT	TAAAGTATA ATACAATACT GGTACAGA AGTTGCAAACT AGTGCTACAA								
2501 ATCTACTAGA TACTGTTGCA GTGGCAGTTG CTAATTGGAC TGACAGCACA	ATCTTAGGCA TACAAAGCAT ACGGAGAGGG ATTTCTTAACA TACCAAGAAG								
2601 GATTAGACAG GGCCTTGAA GACTCCTGTT A									

FIG. 6

1 GCAGAGACAG GACAGGAAC TGCCTACTTC CTGTAAAT TAGCAGCAAG ATGGCCTATT AAAATACTAC ATACAGACAA 80
81 TGGGCCCTAAC TTTACAAGTG CAGCCATGAA AGCTGCATGT TGGTGGACAA ACATACAACA TGAGTTTGA ATACCATACA
161 ATCCACAAAG TCAAGGAGTA GTAGAAGCCA TGAACAAGGA ATTAAATCA ATCATACAGG TGAGGGACCA AGCAGAGCAC
241 TTAAGGACAG CAGTACAAAT GGCAGTATTT GTTCACAATT TTAAGAAGAA AGGGGGGATT GGGGGGTACA CTGCAGGAGA
321 GAGATTAATA GACATATTAG CATCACAAAT ACAACAACA GAACACAAA AACAAATTTT AAAAATTCAA AATTTTCGGG
401 TCTATTACAG AGACAGCAGA GACCCTATTT GGAAAGGACC GGCACAGCTC CTG 60 70 80

FIG. 7

	<u>GAG REGION</u>					
	#	#	#	#	#	#
DUR	qgqmvhqal	sprtl	nawvkaveekafn	peipmfmalsegavpydin	vmnlai	gghqgal
ANT	-----i	-----i	-----i	-----i	-----i	-----t
MVP	-----i	-----i	-----i	-----i	-----i	-----t
LAI	-----i	-----v	-----s	-----v	-----t	q-l-t
MAL	-----i	-----vi	-----s	-----v	-----t	q-l-m
CPZ	-----i	-----v	-----s	-----v	-----l	q-v-t
						-----v
						-----m

FIG. 8A

q
p
r
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s
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n
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h
e
f
o
l
l
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w
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m
a
t
i
o
n

	#	#	#	#	#
DUR	qvl	ke	in	de	aa
ANT	dr	ah	pp	gg	ir
MVP	ep	ve	tt	pp	gg
LAI	ir	ep	tt	st	st
MAL	di	ag	tt	st	st
CPZ	qg	il	wt	tr	ag

FIG. 8B

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HIV1-M / HIV1-O DISCRIMINATING POSITIONS : #

HYPERVARIABLE REGIONS : |||||

FIG. 8C

REGION OF THE V3 LOOP OF GP120

---YK---QRTG- ---Q-LY- THR-I-DI ---	MAD
CTRPNNTRKSIRIQRCGRAFTV IGK IGNM ROAHC	LAI
-----NR-S-----H-- TKQ-I-DI -----	OYI
-A--YQ---QRTP- -L-QSLY- TR SRSII G----	ELI
---G---RGIHF ---QALY- T- -V-DI -R-Y-	MAL
-S--Y-TRKNIRRYSI-S-QAFYV T---I-DI -Q---	455
-H--G-----GE VQI---MTFYN -ENVV-DT -S-Y-	CPZ
-E--QI DIQE MRI-- M-WYSMG--GTA--S S---Y-	ANT
-I-EGIAEVQD-YT -- MRWRSM TLIRSNNT S-V-Y-	MVP
-E--G-QTIQK-MA -- M-WYSMALSN TK-DT -A-Y-	VAU
-V--G--SV-E-K- -- M-WYSMQ-EREGKGANS-T-F-	DUR
C*R*****I****GP M*W*SM*****SR*A*C HIV-O CONSENSUS	
CVRPGNNSVKEIKI GP_MAWYSMQIEREGKGANSRTAF_C	DUR

FIG. 9A

IMMUNODOMINANT REGION OF GP41
[~~~~~]
[=====]

MAD	-V--Q--H--T--S--
LAI	RILAVERYLKDQQLGIWGCSGKLICTTAVPWNASWS
OYI	-V-----T-----
ELI	-----H--N--S--
MAL	-V-----Q--R--M--H--F--S--
455	-V-----Q-----T-----S--
CPZ	-L-----Q--I--L-----AV-Y-T--N--P
ANT	-L--L-TL-QN---SL--K---V-Y-S-K--RT-I
MVP	-LQ-L-TLIQN--R-NL--K-----Y-S-K--RT-I
VAU	-L--L-TFIQN---NL---KNR---Y-S-K--KT-G
DUR	-L--L-TLMQN---NL---R--A--Y-S-Q--ET-G
HIV-O	CONSENSUS RL*ALET**QNQQ*L*WGC*****CYTSV*WN*TW*
DUR	RLLALETLMQNQQQLLNWGCGRGKAICYTSVQWNETWG [.....]

FIG. 9B

FIG. 10

CAGGACAAATGGTACATCAGGCCATCTCCCCAGAACTTTATATGTATGGGTAAAGGCA
GTAGAAAGAAAGGCCTTTAAACCTGAAATTTATCCCTATGTTTATGGCACTATCAGAAGGA
GCTGTTCCCTATGATATCAATGTTATGCTAAATGCCATAGGAGGACACCAAGGGCTTTA
CAAGTATTAAAGAGTAAATCAATGATGAAGCAGCAGACTGGGATAGAGCTCACCCACAA
CAGGAGGGCCGTTACACAGGCGAGATAAGGGAACCAACAGGAAGTGACATTGCTGGA
ACAACTAGCACACAGAAAGCAAAATCTCTGGACTACTAGGCGAGTAACCCATCCCCA
GTTGGAGACATCTATAGGAAATGGATAGTGTGGTCTAAACAAAATGGTAAAAATGTAT
ACTCCAGTGAGCATCTTAGATATTAGCAGGACCAAAAGAACCATTTAGAGATTATGTA
GACAGGTTCTACAAACATTAAGAGCTGAGCAG

GAG REGION OF HIV1-0 DUR STRAIN: 513 BASE PAIRS

= SEQ ID N° 9

QGMVHQALSPRTLNAWVKAVEEKAFNPEIIPMFALSEGAVPYDINVMLNAIGGHQAL
QVLKEVINDEAADWDRAHPQAGPLPPGQIREPTGSDIAGTTSTQEQEILWTTTRAGNPIP
VGDIYRKWIVLGLNKMVKMYSFVSILDIRQGPKEPFRDYVDRFYKTLRAEQ

GAG REGION OF HIV1-0 VIRUS DUR STRAIN: 171 AMINO ACIDS

FIG. 10

FIG. 11

ATTCCAATACACTATTGTGCTCCAGCAGGATATGCTATCTTTAAATGCAACAACGAGGAG
TTTACTGGAAGGCCCATGTAACAACATTTTCAGTAGTTACCTGTACACAGGGTATCAAG
CCAAAGTAAGCACTCATCTAATATTCAATGGGACAATCTCTGAAAGAAAAATAAGAATT
ATGGGAAAGAACATCTCGAGCACTCAGGTAATATCCTAGTGACCCCTAAATTTCTACTATA
AACATGACCTGTGTGAGGCCAGGAAATAATTCAGTACAGGAGATAAAAATAGGTCCAATG
GCTTGTACAGTATGCAAAATTGAGCGAGGGGAAAAGGAGCAAAATTCAGAACAGCTTTT
TGTACCTATAATGCCACGGACTGGAGAAAAACCTTGCAAGGATAGCTGAAAGGTATTTA
GAACTTGTAATAAAACAAGTCCGACTGAATAATGTTCAATAAAAGCAATGGTGGAGAT
GCACAAATAACCCGTTTGCAATTTAACTGTCATGGAGAAATTCCTTT

V3 LOOP OF GP120 DUR STRAIN: 525 BASE PAIRS

= SEQ ID N° 10

IPIHYCAPAGYAIFKCNNEEFTGKPCNNISVVVTCTQGIKPTVSTHLIFNGTISERKIRI
MGKNISSNSGNILVTLNSTINMTCVRPGNNSVQEIKIGPMAWYSMQIEREGKANSRTAF
CTYNATDWRKTLQGIERYLELYVNKTSPTEIFMKNKSNGGDAEITRLHFNSCGEFF

V3 LOOP OF GP120 DUR STRAIN: 175 AMINO ACIDS

FIG. 11

ATAGTGCAACAGCAGGACAAACCTGCTGAGAGCAATACAGGCCAGCAACATCTGCTGAGG
TTATCTGTATGGGGTATTAGACAACCTCCGAGCTCGCTGCTAGCCTTAGAAACCCCTTATG
CAGAAATCAGCAACTCCTAAACCTGTGGGTTGTAGAGGAAAAGCAATCTGCTACACATCA
GTACAATGGAAATGAACATGGGGAGGAAATGACTCAATTTGGGACAGGTTAACATGGCAG
CAATGGGATCAACAGATAGCCCAATGTAAGCTCTTTATATATATGACAAAATACAAGAAGCA
CAAGAACAA

DNA SEQUENCE OF THE IMMUNODOMINANT REGION OF GP41 OF
HIV1-O DUR: 312 BASE PAIRS

= SEQ ID N° 11

IVQQQDNLRLRAIQQQHLLRLSVWGIRQLRARLLALEILMQNQQLNLNWGCRGKAICYTS
VQWNETWGGNDSIWDRLTWQQWDQQIANVSSFTYDKIQEAQEQQ

DNA SEQUENCE OF THE IMMUNODOMINANT REGION OF GP41 OF
HIV1-O DUR - PREDICTED PROTEIN: 104 AMINO ACIDS

FIG. 12

SPECIFIC PRIMERS OF THE HIV-O TYPE

DUR V3a	ATT-CCA-ATA-CAC-TAT-TGT-GCT-CCA-3'
DUR V3r	AAA-GAA-TTC-TCC-ATG-ACT-GTT-AAA-3'
DUR 41a	GGT-ATA-GTG-CAA-CAG-CAG-GAC-AAC-3'
DUR 41r	AGA-GGC-CCA-TTC-ATC-TAA-CTC-3'

FIG. 13A

POSITIONS OF THE PRIMERS:

IN HIV MVP5180

dur V3a	6896 TO 6919
dur V3r	7400 TO 7423
dur 41a	7934 TO 7957
dur 41r	8292 TO 8302

IN HIV ANT70

dur V3a	6896 TO 6920
dur V3r	7392 TO 7415
dur 41a	7917 TO 7940
dur 41r	8256 TO 8276

IN HIV1 VAU

dur V3a	640 TO 663
dur V3r	1138 TO 1161
dur 41a	1684 TO 1707
dur 41r	2026 TO 2046

FIG. 13B

V3	
HIV1-M CONSENSUS	NEGATIVE
HIV1-M MAL (AFRICAN)	NEGATIVE
HIV1-M CTV-CPZ (CHIMPANZEE)	NEGATIVE
HIV1-O MVP5180	NEGATIVE
HIV1-O ANT70	POSITIVE

GP41	
HIV1-M CONSENSUS:	
-PASTEUR STANDARD	NEGATIVE
-INNOGENETICS RIGHT-EXTENDED	WEAK POSITIVE
HIV1-O MVP5180:	
-INNOGENETICS	NEGATIVE
-BEHRING LEFT-EXTENDED	POSITIVE
HIV1-O VAU	POSITIVE

FIG. 14

NUCLEOTIDE COMPARISONS
 EXPRESSED AS PERCENTAGE DIFFERENCE

GP41 (OUT OF 330 BASES)

LAI	0						
MAL	11	0					
CPZ	33	31	0				
MVP5180	39	38	38	0			
ANT70	36	39	37	15	0		
VAU	39	38	38	14	14	0	
DUR	38	36	37	13	15	11	0
	LAI	MAL	CPZ	MVP	ANT	VAU	DUR
				5180	70		

FIG. 15A

V3 (OUT OF 558 BASES)

LAI	0						
MAL	19	0					
CPZ	37	34	0				
MVP5180	46	43	45	0			
ANT70	45	44	43	23	0		
VAU	44	41	41	24	24	0	
DUR	46	43	42	25	22	24	0
	LAI	MAL	CPZ	MVP	ANT	VAU	DUR
				5180	70		

GAG (OUT OF 520 BASES)

LAI	0						
MAL	9	0					
CPZ	21	25	0				
MVP5180	24	26	25	0			
ANT70	25	25	24	10	0		
DUR	25	26	25	9	10	0	
	LAI	MAL	CPZ	MVP	ANT	DUR	
				5180	70		

FIG. 15B

PROTEIN COMPARISONS
 EXPRESSED AS PERCENTAGE DIFFERENCE

GP41 (OUT OF 109 AMINO ACIDS)

LAI	0						
MAL	17	0					
CPZ	33	28	0				
MVP5180	42	40	41	0			
ANT70	42	45	39	22	0		
VAU	44	47	45	19	21	0	
DUR	44	42	39	17	17	14	0
	LAI	MAL	CPZ	MVP	ANT	VAU	DUR
				5180	70		

FIG. 16A

V3 (OUT OF 186 AMINO ACIDS)

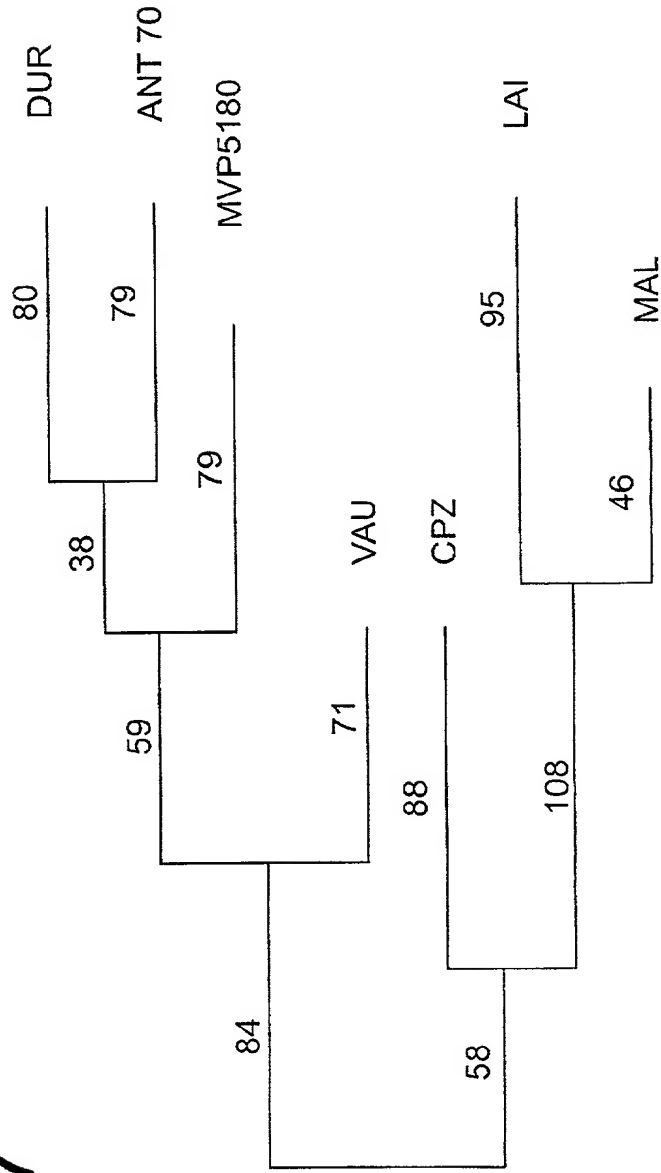
LAI	0						
MAL	31	0					
CPZ	46	39	0				
MVP5180	55	50	59	0			
ANT70	55	50	55	36	0		
VAU	55	51	55	39	36	0	
DUR	56	51	56	39	35	42	0
	LAI	MAL	CPZ	MVP	ANT	VAU	DUR
				5180	70		

GAG (OUT OF 174 AMINO ACIDS)

LAI	0						
MAL	6	0					
CPZ	11	14	0				
MVP5180	21	23	18	0			
ANT70	21	24	19	6	0		
DUR	22	22	19	7	9	0	
	LAI	MAL	CPZ	MVP	ANT	DUR	
				5180	70		

FIG. 16B

FIG. 17



PHYLOGENETIC TREE OF V3
(TREEALIGN PROGRAM, J. HEIN, ON BISANCE, CIT12)
(OUT OF 171 AMINO ACIDS)

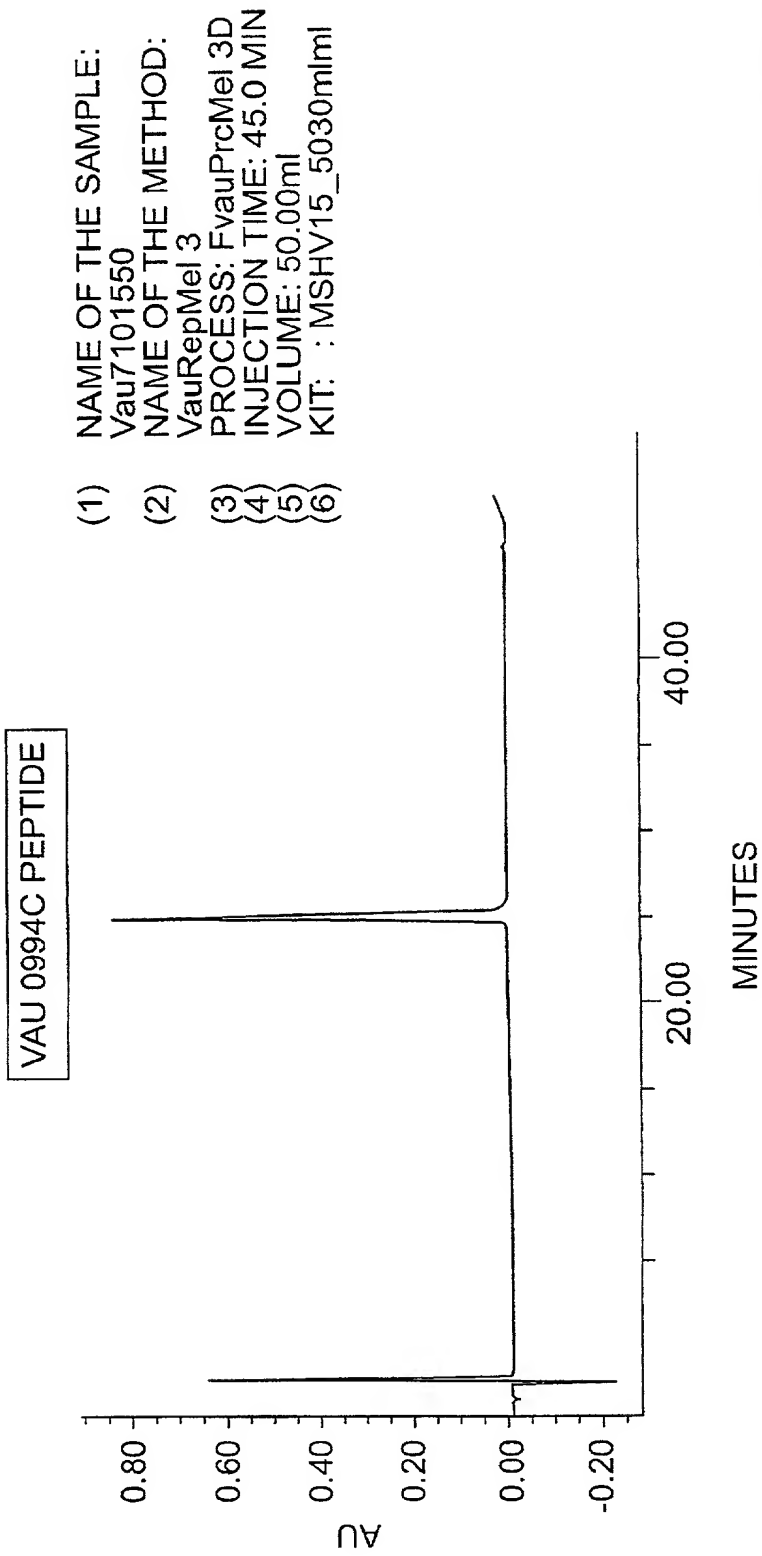
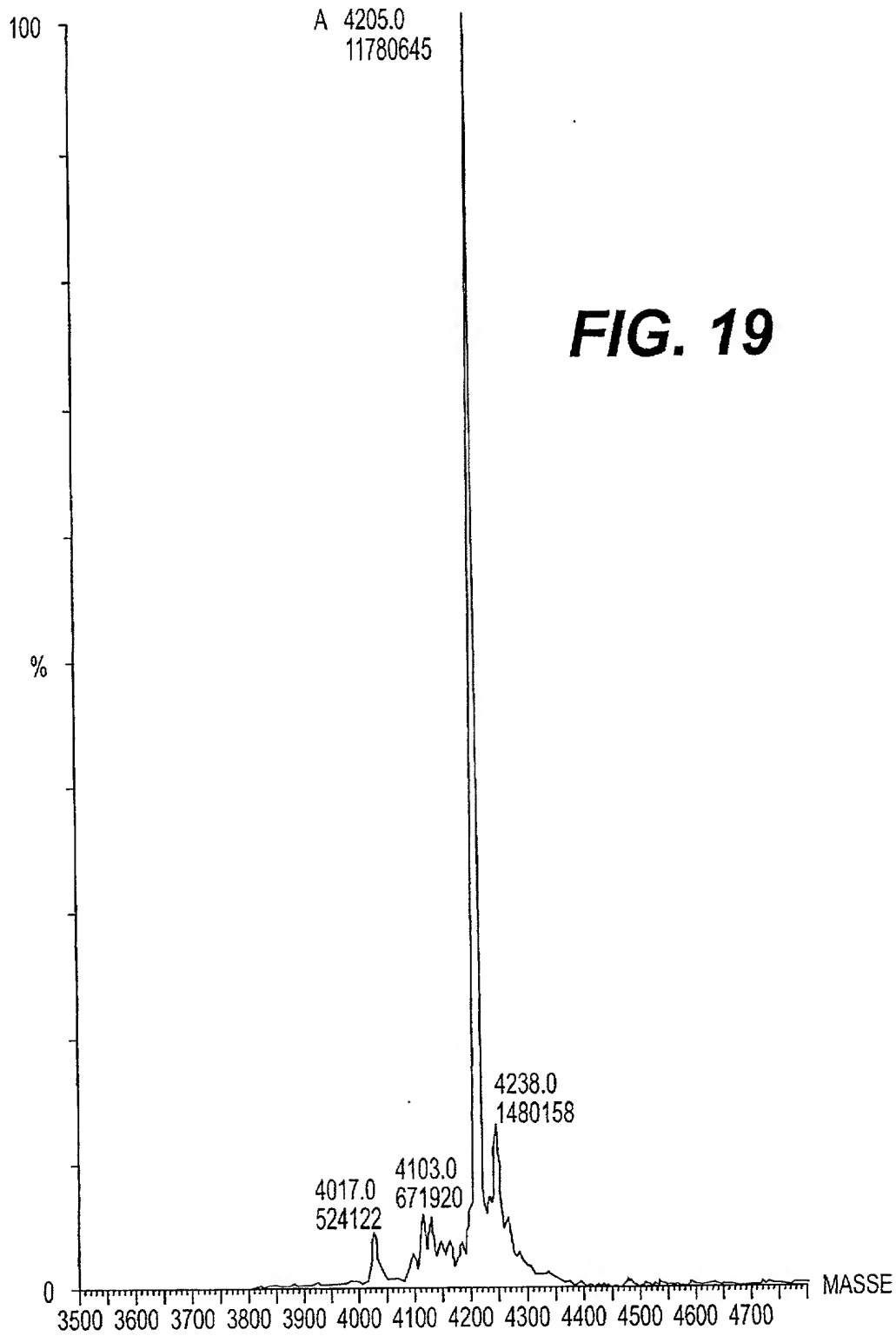


FIG. 18A

CHROMATOGRAPHIC RESULTS

RETENTION TIME (MIN)	INITIAL TIME (MIN)	FINAL TIME (MIN)	% SURFACE AREA	INT TYPE
24.482	23.898	24.932	100.00	BB

FIG. 18B



VAU PEPTIDE

REF: F VAU 0994 C 710

SEQUENCE: RLLALETFIQNQQLLN**WGCKNR**LICYTSVKWNKT

LENGTH: 35

MOLECULAR WEIGHT: 4210

ANALYTICAL CONTROLS: > 95% BY HPLC AND MASS SPECTROMETRY

FIG. 20

STUDY OF THE IMMUNOREACTIVITY OF THE PEPTIDE
 MIMICKING THE IMMUNODOMINANT EPITOPE OF THE
 GP160 VAU SEQUENCE (SUBTYPE O)

VS=0.1 RATIO	VAU PEPTIDE 2µg/ml
<u>HIV1 SERA (PANEL BBI)</u>	
BO1 NO° 12	0.80
BO1 NO° 13	0.40
BO1 NO° 15	0.80
PRB911K6	0.20
<u>HIV1 SERA (ROMANIA)</u>	
<u>STAGE 3/4</u>	
3989	9.50
5116	8.60
<u>HIV1 SERA (PANEL AFM)</u>	
<u>SUBTYPE O</u>	
MAA	>30
LOB	>30
HAM	>30
DUR	12.50
<u>HIV1 SERUM (REIMS)</u>	
<u>SUB TYPE M?</u>	
MAD	0.20

FIG. 21A

<u>SUSPICION OF SUBTYPE O</u> <u>(YAOUNDE PASTEUR CENTER)</u>	
	0.60
3372	>30
3361	28.80
1507	28.70
3167	>30
2628	28.10
1060	0.60
4020	0.30
4783	0.30
5322	0.40
6661	0.50
5527	0.30
5863	25.00
5969	>30
6487	>30
6509	0.70
6782	>30
5453	27.30
3826	1.50
<u>HIV2 SERA</u>	
BERT	0.30
PAOL	4.50
RIV	15.80

INDIRECT EIA PROCEDURE; 3 X 30 MIN TYPE GENELAVIA MIXT

NEGATIVE SERA	
N=48 AVERAGE	0.022
DS AVERAGE	0.007
+12DS	0.107
VS	0.100

FIG. 21B

SUMMARY OF THE RESULTS OBTAINED ON THE AFRICAN SERA

	WB1 RESULTS									
	GP 160	GP 120	P 68	P 55	GP 41	P 40	P 34	P 25	P 18	
3361	++	+-	+				++	+	+	POS
1507	+	+-					+-	+-		POS
2628	+-		++	++		+	+	++	++	POS
3167	++	+	++	++	+	+	++	++	++	POS
3372	++	+-	+	++	+	+	++	++	+-	POS
5453	++	+-	+	+	+-	+	+	+	+	POS
5863	++	+-	+	+	+-	+-	+	+	+	POS
5969	+-		+	+		+	+	+		IND
6487	++		+	+			+	+-	+-	IND
6782	++		+	+	+	+	+	+		POS
950	+-		+-				+-	+-	+-	IND
1060	+-							+-	+	IND
5527										?
6509	++		+-				+-			IND
6661	+							+		IND
4020=	+							(+-)		IND
SEMT										
4783=	+-							+-	+-	IND
5322										
3826								+-	+-	IND
MAD	++	+	+	+	+	+	+	+	+	POS
DUR										
MAA										
LOB	+		++	+-			++	++		IND
HAM			+				+	+		IND

=RATIO<1
 =RATIO>2

FIG. 22A

	TEST DE SCREENING (RATIO : DO/VS)				
		GEM IND HIV1+2	ABBOTT SDW HIV1+2	MUREX SDW HIV1+2	
3361	0.10	18.00	0.56	0.72	1.40
1507	0.97	14.25	3.03	5.35	0.98
2628	0.70	18.00	4.84	1.71	1.34
3167	0.38	18.30	11.89	>6	0.88
3372	0.19	16.80	11.63	3.76	0.47
5453	2.50	>20			1.70
5863	2.30	>20			1.90
5969	2.30	15.20			2.25
6487	0.32	19.70			1.90
6782	0.07	13.40			2.95
950	1.20	6.00	5.76	>6	0.68
1060	0.60	18.00	0.46	1.25	0.67
5527	0.27	2.40			0.52
6509	0.32	>16			2.14
6661	8.10	10.10			1.54
4020= SEMT	0.23	6.30	1.03	4.98	4.12
4783= 5322	0.19	8.10 10.90	0.41		0.55 0.52
3826		3.93		1.64	0.72
MAD	-	+	+		
DUR		>8	2.00	0.80	
MAA					
LOB		>19	2.00	2.70	1.50
HAM		>19	1.80	7.80	2.70

FIG. 22B

	EIA PEPTIDES							
	CLONATEC RAP HIV1	39D6 HIV1B	FER HIV1B	39A HIV1B	VAU HIV1O	MVPP 5180 HIV1O	BNR 19 HIV1O	PEPTI- LAV1-2
3361	+				28.8	25.80	NT	
1507	DUBIOUS			8.4	28.7	28.80	1.7	
2628				3.6	28.1	19.30	1.2	
3167	+			>30	>30	>30	1.6	
3372	+/-			2.8	>30	24.00	4.9	
5453	-	4.36	1.37	3.6	27.3		1.6	-
5863	-	1.42	0.40	1.4	25		0.5	-
5969	-	0.94	1.90	19.4	>30		0.6	+
6487	+	25.75	5.76	>30	>30		0.7	
6782	-	0.64	0.49	0.8	>30		10.3	-
950					0.6		0.4	
1060	DUBIOUS			1.9	0.6	0.40	0.6	
5527	-			4.5	0.3		0.2	+/-
6509	+			16.9	0.7		0.2	
6661	+			2.8	0.5		0.4	
4020=	?Ag-			1.15	0.3		0.5	
SEMT				1.2	0.7		0.9	
4783=				2.5	0.3		0.3	
5322				4	0.4		0.3	
3826				1.6	1.5		0.7	
MAD		0.66	2.72	26.7	0.2		>30	-
DUR		>30	>30	>30	12.5		0.2	
MAA				NT	>30		NT	
LOB		1.02	5.62	12.5	>30		>30	
HAM		0.73	0.41	13.3	>30		0.7	

FIG. 22C